

Fig. 1

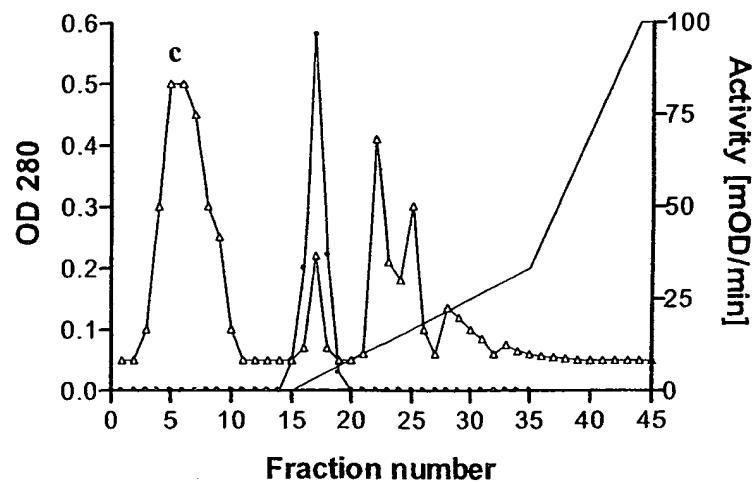
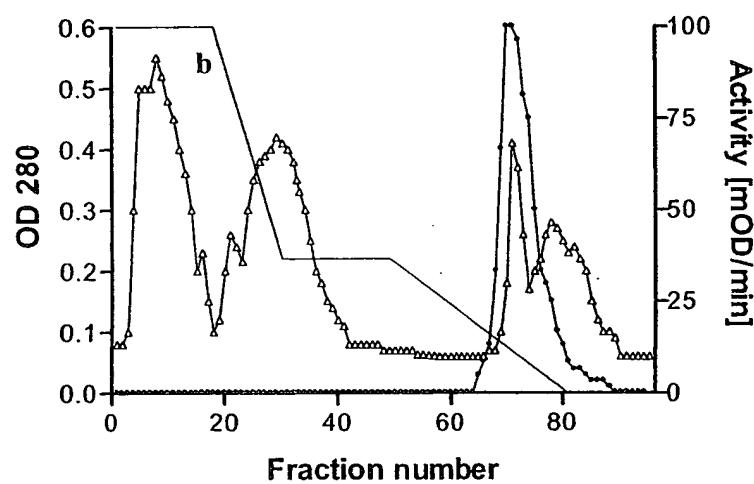
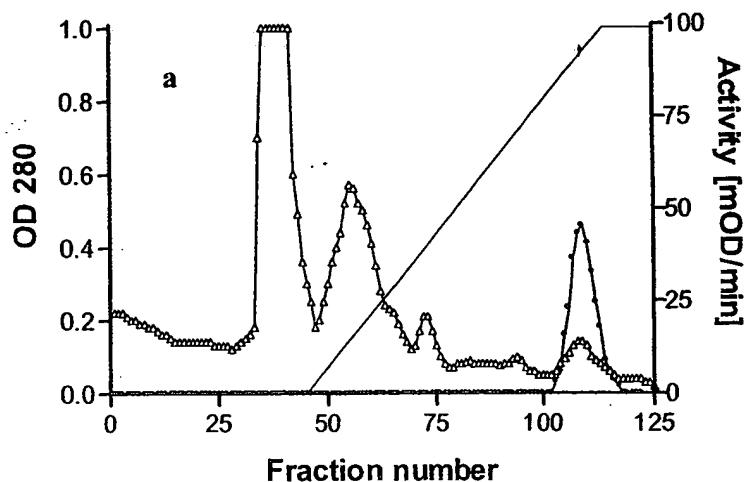
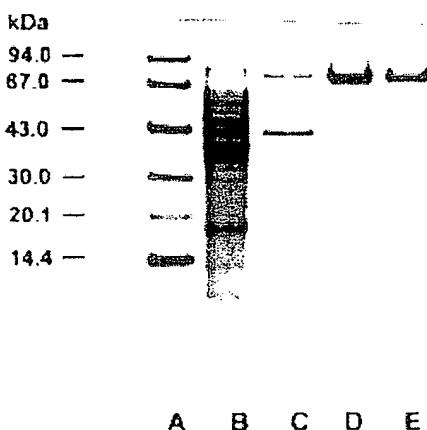


Fig. 2



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Fig. 3

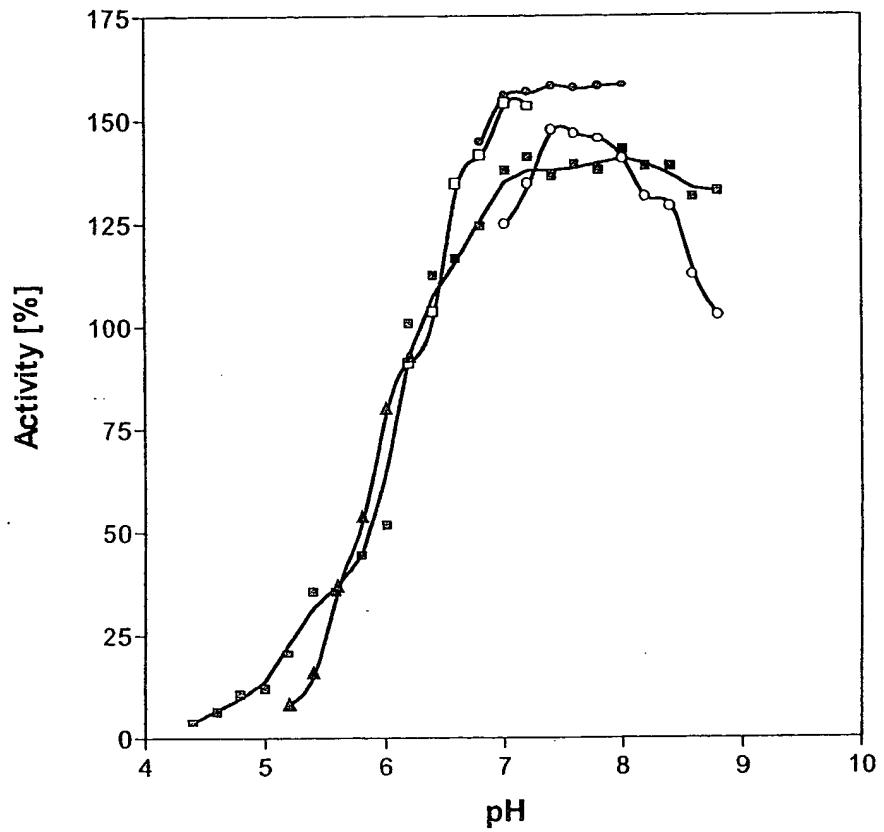


Fig. 4

Fig. 5

FIGURE 5 SEQ ID N

SEQ ID NO.3 DPP-7

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TGGNSGSPVFT++ +IG+ + G + G + + + + I + F  
704 TGGNSGSPVFNENKNEVIGHWGGVPNEFNGAVFINENVRNFLKQNIEDIHFA863

SEQ ID NO.4 V-8

Fig. 6

Title: DIPEPTIDYLPEPTIDASES AND METHODS OF USE  
 Applicant(s): Travis et al.  
 Filed: HEREWITH  
 Express Mail No.: EL888272705US

Docket: 235.0044 0101  
 Sheet 6 of 7

SEQ ID NO: 5 S1 1 MASQALGFLHQNGINTKKWLTISVAVASFASHADEGMWOPHOLP-AMADVALKAKLEIDAKSIISKLTIEPNN--AVISL  
 SEQ ID NO: 6 S2 1 -----MRLALVAVIYLTCGATATADECQWQPYOMP-STADKLSARCDIDPAKDLTSPVN--AVWL  
 SEQ ID NO: 7 X 1 -----MRNFTLTSVLAATITVDSTHAGCMMWYQOLP-ELAGPTKOACIQSPQIQLSNLTGDPNG--AVWSL  
 SEQ ID NO: 8 P1 1 -----MOKLKSITGAALHGSAGVAKADKGMTINELNOENTDRMRELGTPIDSYSEDKPSTANAVIFG  
 SEQ ID NO: 9 P2 1 -----MKKRMHILPFAVCLCQIQAHADEGMWIMQOLG-RKYAQMKERGKIKYEDLYNPNGTISKDAVILFD

S1 78 GGCTASFVSPKGLVWINTNHCAYGSIONNSTPEKNULODGETAKTFADELPAAPGSRVWTEDVINVTERVRKGLENKTG-  
 S2 62 CYCTASFVSPQGLVWINTNHCAYGKATQNTKKEHNYLEOGETAATSMDEPSAGPNERJNTTEAMVUDVTSVTKDLSODP--  
 X 66 GNCTASTVSPECGLVWINTNHCAYGKATQNSTPKNLTKEGENALTOADEVSAGPNAJWLEQITDVTQAKZALAVAGND  
 P1 71 GCCTGTTVSDQGLTETNHHCYGAQIQSOSTVHDYKRDGFWSRPM-ELPIPIGLSVKTRKIVKVTDPKECOKGKTD-  
 P2 67 GGCTGEVVSDRGLVLTINHCGYDMDIQAHSTLEHNYLNGEWANREA-ELPNKDISVFLDKIEDVTDVYKVDKOP

S1 157 -----REFYQGVENOEKALVAECEKDEGYRCQYSEHGGIEKLYKQLEIRDVRLVNFAGSVKQGGDWDNMMWPRHT  
 S2 140 -----IKRYEELEJENHSKALIKSCEADDNYRCNVRSEHNGLEKQFIAATSMDEPSAGPNERJNTTEAMVUDVTSVTKDLSODP--  
 X 146 -----PFKRTTAEFTSKOETAKCEEEOGYRCOFFSFAGGNTYREVKNELEKDVRLVYAPOGSVCKFECCDDTDNMMWPRHT  
 P1 149 -----EMERLKAQEVCOEJAKKENADENOCLTVEPFYNNVVELTIVDVEKDVRMVEAPPSSVCKFECCDDTDNMMWPRHT  
 P2 146 NSMDYLVSPKLYOKLADKAKGKNEFSAKNGLSVELKAFYGGNTYLMFTKTYTDVRLVGAPPTSIGKFGADTDNMMWPRHT

S1 231 GDYSEFWRAYVSKNGKPAEESADNMPPEPKSFLKVSAGVSEGEDEVVAGYPGRTRNRYRATAVEVONEEEWAWPEGKMRER  
 S2 214 GDFAAFTRAYVCKOCKPAAFSEDNTPYLPSYKLVNADGVKAGDGVWAGYPGRTRNRYRATAVEVONEEEWAWPEGKMRER  
 X 221 GDFSEFWRAYVCKOCKPASEFSKENTPYRPHWIKBSPDOPGIDCDEVMWAGYPGRTRNRYRATAVEVONEEEWAWPEGKMRER  
 P1 224 GDFSEFWRAYVCAJNRPAEYSKDNKPYKPYFAAVSMOCYKADDYAMTICPCPSTDRYLTSGWVEDRIENENPRIELVRCI  
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S1 311 FIEKIKATAPEGSDERIKEFOTAGIANYARNFTSMIEFICKSTMLADKALEAKLAEMIADSS--REAKYKTLAE  
 S2 294 QIDTHEAMGQKDAIDIAIKKAGNMASSMANMRKINGLLAGERKATDINGIKOORENDEFLAWLTKPN-----LNLNLSL  
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 P1 304 KOCHIKEAMSADQATRIKYASKYAOQSEANYWKNISIGNRCLARLDVICKRRAEEERAADWIRKNCYKSAV---YGDVLSLE  
 P2 306 RQGVWLMELADPOIKIMYSAKYMASONAKRAICANWAIKTRGRJTRQNKQAMODRINTAWGAKQCTP-----RYEEAVHE

S1 388 DALIASKSKAHOERDMITSVYISSTTMPTANLNLXRLAHEKOLPDMOREPGEQDRDMTRFKASERIDRRAASVDKAVLFD  
 S2 368 EVLVAEOOLOTOINTYFTNAOSSIMLTAANNLRLAKEOKSDAERIEQYERDAMFSSRKLKIDSSEPDVKVDTKTLQ  
 X 378 VDLTEQYKANODRDEVIGQENGSCVIGVAVNLYRLAERTKSDAOREAGYQERDIPTEGNIKOMERRYLPEMDROMQOY  
 P1 381 KAYKEGAKANREMTYISETLEFGCTEVVRAFAQFANALATNPDAAHAGILKSDDKYKYLPSLDRKVLPAMLDIVRRRIPAD  
 P2 380 IDATVAKRADIRRYMIELEGIRGIEFARSPPISTEDETAKLOGNDASARKEAIDKIRTRYSKFANKDYSAEVDKKWAV

S1 468 MIKRIAAALPAAQRIIPAMDKAFCIDNKNEAKLAKTIDKMKAYTEIGNKDVRЛАММЕКSVDDFKASKDPEIPEAVAMYDIN  
 S2 448 DILN-AVLSOPNRAVADINMNLNDKN--VSLAAKLDGLYSLITITDQAORLAWMADAKAETSSDPEIIRIJAVAIDIN

X 458 WITFENKILPKVORYAATDVMWEDCIRAT-----I-KLGDKISSSERIKMENADRAFESSODPATRZAVANP  
 P1 461 KUPDFKVKVIDKFKGDTKVKYDFVFD--KS-----VVPSDKFHAMTKSMKEKEAKAEKDPAVELSKVIAA  
 P2 460 MLLTEYLKEIPYENIPLHLRLVMDRFG----DVQAVVDDIFARSVFGSQAQFDAAIVPSVEKLKEDPMALAESVDEY

S1 548 WSEERKEELDCELMVYRPOYDANIAHNEOCKPVIAADANSSRIVVGHVKGYSPKDGVAVPFTREGEVORDIG-ID  
 S2 524 MAOEKAETKLACKLSTARPAYMAAVDYYKANNWPVYDANGTLRISYGMVDDYQOSRDAKYKOPETRDLGIVAKHIC-VE  
 X 530 PETERONKIRTCELIKARPITVQALADYNKSHICKEVYDANSSTRTECHVKKYSPKDGVETPFTLQWAKNTC-VE  
 P1 530 RAJADAMANAYAIEKGSKRLEAGIREMYP--GRALPSDANEITMRMSYGSIKGYEPDCAYVNYHTTGKGYTEKQDPKS  
 P2 536 RKLYNELRPPYDDPILRAORTYIAGILEMDG--DQDQEPDANITLRFETYGQVKGYSPRDNWYIHQHTLDGYMEKEDPDNW

S1 627 PDAPKQOLMTEKOKOYGDYMKSIDS-----VPVNFLSIEDTTGGNSGSPTINGRAELVGLIE  
 S2 603 PYNAPKKLIDALTSVORFEDHLYVSYDPRGWICRLFSCLDKPEEFNSVPVNFLSSVDTTGGNSGSPTVENGKELVGLIE  
 X 609 PFDPSKSLNIAKSYANTADORTIGT-----VPVNFLSIEDLTGGNSGSPTVDAHCKLVLGIAF  
 P1 608 EEAIVOENLTIDFERTKNGYRGAENGQOLH-----IAF--LSNDITGGNSCSPVEDKNCRLTICAF  
 P2 614 EEEVVDPKLKAIVWERKDFERIYADRSGRMP-----VAFCAATHITGGNSGSPTVDAHCKLVLGIAF

S1 686 DGVYESTIGGNAEDNETINRSIHVDSSRYMLWVVKYLDHADNLAELEMETVN-  
 S2 683 DSTYEATTKDNEENPTITRAVHDTIYILWVDEVDHADNLKEDDIDVRN  
 X 668 DGNWESVSSNWWFDPVWVMTAVDSRYVQWMTTEVAAPAHILKEINLYR-  
 P1 665 DGNWEAMSGDIEFEDLQRTISVDIYVLFEMIDK  
 P2 672 DRNWEVGEGDIOXLAQDVKRSIIVDIRVYLVIDKVYGGCQRLDEMIVP-